WHAT IS CLAIMED IS:

1. A method for detecting multiple reiterated oligonucleotides from a target DNA or RNA polynucleotide, said method comprising:

(a) hybridizing an initiator with a single stranded target polynucleotide

(b) incubating said target polynucleotide and initiator with an RNA-polymerase, and a terminator;

(c) synthesizing multiple oligonucleotides from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple reiterative oligonucleotides; and

(d) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts of a polynucleotide of interest.

2. The method of claim 1, further comprising detecting or quantifying said reiteratively synthesized oligonucleotide by modifying a nucleoside or nucleotide in at least one of the members selected from the group consisting of said terminator, and said initiator.

3. The method of claim 2, wherein said modifying comprises incorporating a label moiety.

4. The method of claim 3, wherein said label moiety comprises a fluorophore moiety.

5. The method of claim 4, wherein said fluorophore moiety comprises a fluorescent energy donor and a fluorescent energy acceptor wherein said moiety is detected or quantified by fluorescence resonance energy transfer.

6. The method of claim 1, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA-polymerase, and a primase.

7. The method of claim 6, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

8. The method of claim 1, wherein said initiator is an RNA primer.

9. The method of claim 1, wherein said initiator comprises a molecule selected from the group consisting of: nucleosides, nucleoside analogs, 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, greater than 250 nucleotides, and nucleotide analogs.

10. The method of claim 1, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides, and about 50 nucleotides to about 100 nucleotides, and greater than 100 nucleotides.

11. The method of claim 1, wherein said incubating further comprises a target site probe specific for a region on said single-stranded target polynucleotide.

12. The method of claim 1, wherein said chain terminator comprises a nucleotide analog.

13. A method of detecting multiple reiterated oligonucleotides from a target DNA or RNA polynucleotide, said method comprising:

(a) hybridizing an initiator to a single-stranded target polynucleotide;

(b) incubating said target polynucleotide and initiator with a target site probe, an RNA-polymerase, and a terminator, wherein said target site probe hybridizes with said target polynucleotide;

(c) synthesizing an oligonucleotide transcript that is complementary to said target site from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript, thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(d) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

14. The method of claim 13, wherein said target site probe size is selected from the group consisting of: about 20 to about 50 nucleotides, about 51 to about 75 nucleotides, about 76 to about 100 nucleotides and greater than 100 nucleotides.

15. The method of claim 13, further comprising detecting or quantifying said reiteratively synthesized oligonucleotide by modifying a nucleotide in at least one of the members selected from the group consisting of said terminator, said initiator, and said target-site probe.

16. The method of claim 15, wherein said modifying comprises incorporating a label moiety.

17. The method of claim 16, wherein said label moiety comprises a fluorophore moiety.

18. The method of claim 17, wherein said fluorophore moiety comprises a fluorescent energy donor and a fluorescent energy acceptor wherein said moiety is detected or quantified by fluorescence resonance energy transfer.

19. The method of claim 13, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA polymerase, and a primase.

20. The method of claim 19, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

21. The method of claim 13, wherein said initiator is an RNA primer.

22. The method of claim 13, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

23. The method of claim 13, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides, and greater than 100 nucleotides.

24. The method of claim 13, wherein said mixture in "a" further comprises a target site probe specific for a region on said single-stranded target polynucleotide.

25. The method of claim 13, wherein said chain terminator comprises a nucleotide analog.

26. A method for detecting methylated cytosine residues at CpG sites in a target polynucleotide, comprising:

(a) deaminating a single-stranded target DNA sequence under conditions which convert unmethylated cytosine residues to uracil residues while not converting methylated cytosine residues to uracil;

(b) hybridizing an initiator with a single stranded target polynucleotide;

(c) incubating said deaminated target polynucleotide and said initiator with a terminator, and an RNA-polymerase, wherein at least one of said initiator, or terminator is modified to enable detection of the CG sites;

(d) synthesizing an oligonucleotide transcript that is complementary to said CG sites from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(e) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

27. A method for detecting methylated cytosine residues at a CpG site in a target gene, said method comprising:

(a) deaminating a single-stranded target DNA polynucleotide under conditions which convert unmethylated cytosine residues to uracil residues while not converting methylated cytosine residues to uracil;

(b) hybridizing a target site probe with said single stranded target polynucleotide,

(c) incubating said target polynucleotide and target site probe with, an initiator, a terminator, and an RNA-polymerase, wherein at least one of said initiator, or said terminator are complementary to the CpG site;

(d) synthesizing an oligonucleotide transcript that is complementary to said target site from said target polynucleotide, wherein

said initiator is extended until said terminator is incorporated into said oligonucleotides, thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(e) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

28. The method of claim 27, wherein said target site probe size is selected from the group consisting of: about 5-19; about 20 to about 50 nucleotides, about 51 to about 75 nucleotides, about 76 to about 100 nucleotides and greater than 100 nucleotides.

29. The method of clam 27, further comprising detecting or quantifying said reiteratively synthesized oligonucleotide by modifying a nucleotide in at least one of the members selected from the group consisting of said terminator, and said initiator.

30. The method of claim 29, wherein said modifying comprises incorporating a label moiety.

31. The method of claim 30, wherein said label moiety comprises a fluorophore moiety.

32. The method of claim 31, wherein said fluorophore moiety comprises one of a fluorescent energy donor and a fluorescent energy acceptor wherein said moiety is detected or quantified by fluorescence resonance energy transfer.

33. The method of claim 27, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA polymerase, and a primase.

34. The method of claim 27, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

35. The method of claim 27, wherein said initiator is an RNA primer.

36. The method of claim 27, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

37. The method of claim 27, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides, and greater than 100 nucleotides.

38. The method of claim 27, wherein said chain terminator comprises a nucleotide analog.

39. The method of claim 26 or 27, wherein deaminating a single-stranded target DNA sequence comprises treating said single-stranded target DNA sequence with sodium bisulfite.

40. The method of claim 27, wherein said target site probe and said target DNA sequence form a bubble complex comprising a first double-stranded region upstream of said target CpG site, a single-stranded region comprising said target CpG site, and a second double-stranded region downstream of said target CpG site.

41. A method for detecting the presence or absence of mutations in a target DNA sequence, the method comprising

(a) hybridizing a target site probe to a single-stranded DNA polynucleotide, wherein said DNA polynucleotide may contain a mutation relative to a normal or wild type gene;

(b) incubating said target polynucleotide and target-site probe with an RNA-polymerase, an initiator, and a terminator;

(c) synthesizing an oligonucleotide transcript from said target polynucleotide that is complementary to a target mutation site, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple abortive reiterative oligonucleotides; and

(d) determining the presence or absence of a mutation by detecting or quantifying said reiteratively synthesized oligonucleotides transcribed from said target DNA polynucleotide.

42. The method of claim 41, wherein said target site probe size is selected from the group consisting of: about 20 to about 50 nucleotides, about 51 to about 75 nucleotides, about 76 to about 100 nucleotides and greater than 100 nucleotides.

43. The method of claim 41, further comprising detecting or quantifying said reiteratively synthesized oligonucleotide by modifying a nucleotide in at least one of the members selected from the group consisting of said terminator, and said initiator.

44. The method of claim 43, wherein said modifying comprises incorporating a label moiety.

45. The method of claim 44, wherein said label moiety comprises a fluorophore moiety.

46. The method of claim 45, wherein said fluorophore moiety comprises a fluorescent energy donor and a fluorescent energy acceptor wherein said moiety is detected or quantified by fluorescence resonance energy transfer.

47. The method of claim 41, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA polymerase, and a primase.

48. The method of claim 47, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

49. The method of claim 41, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides, and greater than 100 nucleotides.

50. The method of claim 41, wherein said chain terminator comprises a nucleotide analog.

51. The method of claim 41, wherein said mutation is selected from the group consisting of: a deletion, an insertion, a substitution, a chromosomal rearrangement, and a single nucleotide polymorphism.

52. The method of claim 41, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

53. The method of claim 41, wherein said target site probe and said target DNA sequence form a bubble complex comprising a first double-stranded region upstream of said target mutation site, a single-stranded region comprising said target mutation site, and a second double-stranded region downstream of said target mutation site.

54. A method for detecting mutations in a target DNA polynucleotide, said method comprising:

(a) immobilizing a capture probe designed to hybridize with said target DNA polynucleotide;

(b) hybridizing said capture probe to said target DNA polynucleotide, wherein said DNA polynucleotide may contain a mutation relative to a normal or wild type gene;

(c) incubating said target polynucleotide with an RNA-polymerase, an initiator, and a terminator;

(d) synthesizing an oligonucleotide transcript that is complementary to a target site from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript, thereby synthesizing multiple abortive reiterative oligonucleotide transcripts; and

(e) determining the presence or absence of a mutation by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts from said target DNA polynucleotide.

55. A method for detecting DNA or RNA in a test sample, said method comprising:

(a) hybridizing a single stranded target polynucleotide with an abortive promoter cassette comprising a sequence that hybridizes to the single stranded target polynucleotide, and a region that can be detected by transcription by a polymerase;

(b) incubating said target polynucleotide with an RNA-polymerase, an initiator, and a terminator;

(c) synthesizing an oligonucleotide transcript that is complementary to the initiation start site of the APC, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides, thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(d) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

56. A method for detecting the presence of pathogens in a test sample, said method comprising the steps of:

(a) hybridizing a single stranded target pathogen polynucleotide in said test sample with an abortive promoter cassette comprising a region that can be detected by transcription by a polymerase;

(b) incubating said target polynucleotide and initiator with an RNA-polymerase, and a terminator;

(c) synthesizing an oligonucleotide transcript that is complementary to initiation start site of the APC, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple abortive reiterative oligonucleotide transcripts; and

(d) determining the presence of a pathogen by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts synthesized from said test sample.

57. The method of any one of claims 54-56, further comprising detecting or quantifying said reiteratively synthesized oligonucleotide transcript by modifying a nucleotide in at least one of the members selected from the group consisting of said terminator, and said initiator.

58. The method of claim 57, wherein said modifying comprises incorporating a label moiety.

59. The method of claim 58, wherein said label moiety comprises a fluorophore moiety.

60. The method of claim 59, wherein said fluorophore moiety comprises a fluorescent energy donor and a fluorescent energy acceptor wherein said moiety is detected or quantified by fluorescence resonance energy transfer.

61. The method of any one of claims 54-56, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA polymerase, and a primase.

62. The method of claim 61, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

63. The method of any one of claims 54-56, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides.

64. The method of any one of claims 54-56, wherein said chain terminator comprises a nucleotide analog.

65. The method of claim 54 or 55, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and

126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

66. The method of any one of claim 56, wherein said single-stranded target polynucleotide is one of DNA and RNA.

67. The method of any one of claims 54-56, wherein said inititator is one of RNA.

68. The method of claim 56, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 25-50 nucleotides, 50-75 nucleotides, 75-100 nucleotides, 100-125 nucleotides, and 125-150 nucleotides, 150-175 nucleotides, 175-200 nucleotides, 200-225 nucleotides, and 225-250 nucleotides.

69. The method of claim 55 or claim 56, wherein said abortive promoter cassette comprises a self-complementary oligonucleotide that forms a single-stranded bubble in the presence of an RNA polymerase, wherein a region of said bubble region can be detected by transcription by said polymerase

70. The method of any one of claim 56, wherein said abortive promoter cassette comprises an APC linker which is adapted to hybridize to an end of said target pathogen polynucleotide.

71. A method for detecting pathogens in a test sample, said method comprising:

(a) immobilizing a capture probe designed to hybridize with a target DNA polynucleotide in said test sample;

(b) hybridizing said capture probe with a test sample that potentially contains said target DNA polynucleotide;

(c) hybridizing a single stranded target DNA polynucleotide in said test sample with an abortive promoter cassette comprising a region that hybridizes to the single stranded target pathogen polynucleotide, and a region that can be detected by transcription by a polymerase;

(d) incubating said target polynucleotide with an RNA-polymerase, initiator, and a terminator;

(e) synthesizing an oligonucleotide transcript that is complementary to said initiation transcription start site of APC, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(f) determining the presence or absence of a pathogen by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

72. A method for detecting mRNA expression in a test sample, the method comprising:

(a) hybridizing a target mRNA sequence with an abortive promoter cassette comprising a region that can be detected by transcription by a polymerase;

(b) incubating said target mRNA sequence with an RNA-polymerase, an initiator, and a terminator;

(c) synthesizing an oligonucleotide transcript that is complementary to transcription initiation start site, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript, thereby synthesizing multiple reiterative oligonucleotides; and

(d) determining the presence or absence of the mRNA by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts synthesized from said test sample.

73. The method of claim 72, further comprising:

(a) immobilizing a capture probe, wherein said probe hybridizes with a target mRNA sequence;

(b) hybridizing said capture probe with a test sample which potentially contains said target mRNA sequence; and

(c) washing a captured target mRNA sequence to remove unhybridized components of said test sample.

74. The method of claim 72, wherein modifying further comprises incorporating an independently selected label moiety into at least one of said initiator, said terminator, and said nucleotides.

75. The method of claim 74, wherein said label moiety comprises a fluorophore moiety.

76. The method of claim 75, wherein detecting comprises detecting by fluorescence resonance energy transfer and said fluorophore moiety comprises one of a fluorescent energy donor and a fluorescent energy acceptor.

77. The method of claim 72, wherein said polymerase is one of a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase, an RNA-dependent DNA polymerase, a DNA-dependent DNA polymerase, and a modified polymerase, and a primase.

78. The method of claim 72, wherein said polymerase comprises an RNA polymerase derived from one of E. coli, E. coli bacteriophage T7, E. coli bacteriophage T3, and S. typhimurium bacteriophage SP6.

79. The method of claim 72, wherein said initiator is one of RNA or DNA.

80. The method of claim 79, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-

75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

81. The method of claim 72, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides, and greater than 100 nucleotides.

82. The method of claim 72, wherein said abortive promoter cassette comprises a self-complementary oligonucleotide that forms a single-stranded bubble region comprising said target site.

83. The method of claim 72, wherein said abortive promoter cassette comprises an APC linker which is adapted to hybridize to a poly-A tail of said target mRNA sequence.

84. The method of claim 72, wherein said chain terminator comprises one of nucleotide deprivation and a nucleotide analog.

85. A method for detecting an oligonucleotide synthesized from a target DNA sequence, the method comprising:

(a) hybridizing a DNA primer with a single-stranded target DNA sequence;

(b) extending said DNA primer with a DNA polymerase and nucleotides, such that said DNA polymerase reiteratively synthesizes a nucleotide sequence; and

(c) detecting oligonucleotide comprised of repeat sequences synthesized by said DNA polymerase.

86. The method of claim 85, further comprising modifying at least one of said DNA primer and said nucleotides to enable detection of said oligonucleotide comprised of repeat sequences.

87. The method of claim 86, wherein modifying further comprises incorporating an independently selected label moiety into at least one of said DNA primer and said nucleotides.

88. The method of claim 87, wherein said label moiety comprises a fluorophore moiety.

89. The method of claim 88, wherein detecting comprises detecting by fluorescence resonance energy transfer and said fluorophore moiety comprises one of a fluorescent energy donor and a fluorescent energy acceptor.

90. The method of claim 85, wherein said DNA polymerase is selected from the group consisting of Escherichia coli DNA polymerase, T7 DNA polymerase, T4 DNA polymerase, Taq thermostable DNA polymerase, terminal transferase, and telomerase.

91. The method of claim 85, wherein said DNA primer comprises from 1 to about 25 nucleotides.

92. The method of claim 85, wherein said oligonucleotide repeat sequence comprises from about 2 to about 26 nucleotides.

93. The method of claim 85, wherein said detecting comprises hybridizing a complementary sequence to the synthesized oligonucleotide comprising repeat sequences.

94. The method of claim 93, wherein said complementary sequence is modified to comprise an independently selected label moiety.

95. The method of claim 94, wherein said label moiety comprises a fluorophore moiety

96. The method of claim 85, further comprising immobilizing said single-stranded target DNA sequence.

97. The method of claim 85, wherein immobilizing comprises hybridizing a capture probe to a portion of said single-stranded target DNA sequence.

98. The method of claim 13, wherein said target site probe and said target DNA sequence form a bubble complex comprising a first double-stranded region upstream of said target site, a single-stranded region comprising said target site, and a second double-stranded region downstream of said target site.

99. A method of producing a microarray, the method comprising:

(a) synthesizing multiple abortive oligonucleotide replicates from a target DNA sequence by the method of claim 1; and

(b) attaching said multiple abortive oligonucleotide replicates to a solid substrate to produce a microarray of said multiple abortive oligonucleotide replicates.

100. The method of any one of claims 4, 17, 31, 45, 75, 88, or 95 wherein said fluorophore moiety is selected from the group consisting of: 4-acetamido-4'-isothiocyanatostilbene-2,2'disulfonic acid; acridine and derivatives: acridine, acridine isothiocyanate; 5-(2'-aminoethyl)amninonaphthalene-1-sulfonic acid (EDANS); 4-amino-N-[3-vinylsulfonyl)phenyl]naphthalimide-3,5 disulfonate; N-(4-amino-1-naphthyl)maleimide; anthranilamide; BODIPY; Brilliant Yellow; coumarin, and derivatives: coumarin, 7-amino-4-

methylcoumarin (AMC, Coumarin 120), 7-amino-4-trifluoromethylcouluarin (Coumaran 151); cyanine dyes; cyanosine; 4',6-diaminidino-2-phenylindole (DAPI); 5', 5"-dibromopyrogallol-sulfonaphthalein (Bromopyrogallol Red); 7-diethylamino-3-(4'-isothiocyanatophenyl)-4-methylcoumarin; diethylenetriamine pentaacetate; 4,4'-diisothiocyanatodihydro-stilbene-2,2'-disulfonic acid; 4,4'-diisothiocyanatostilbene-2,2'-disulfonic acid; 5-[dimethylamino]naphthalene-1-sulfonyl chloride (DNS, dansylchloride); 4-dimethylaminophenylazophenyl-4'-isothiocyanate (DABITC); eosin and derivatives: eosin, eosin isothiocyanate; erythrosin and derivatives: erythrosin B, erythrosin, isothiocyanate; ethidium; fluorescein and derivatives: 5-carboxyfluorescein (FAM),5-(4,6-dichlorotriazin-2-yl)aminofluorescein (DTAF), 2',7'-dimethoxy-4'5'-dichloro-6-carboxyfluorescein (JOE), fluorescein, fluorescein isothiocyanate, QFITC, (XRITC); fluorescamine; IR144; IR1446; Malachite Green isothiocyanate; 4-methylumbelliferoneortho cresolphthalein; nitrotyrosine; pararosaniline; Phenol Red; B-phycoerythrin; o-phthaldialdehyde; pyrene and derivatives: pyrene, pyrene butyrate, succinimidyl 1pyrene; butyrate quantum dots; Reactive Red 4; rhodamine and derivatives: 6-carboxy-X-rhodamine (ROX), 6-carboxyrhodamine (R6G), lissamine rhodamine B, sulfonyl chloride rhodamine (Rhod), rhodamine B, rhodamine 123, rhodamine X isothiocyanate, sulforhodamine B, sulforhodamine 101, sulfonyl chloride derivative of sulforhodamine 101 (Texas Red); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); tetramethyl rhodamine; tetramethyl rhodamine isothiocyanate (TRITC); riboflavin; rosolic acid; terbiun chelate derivatives; Cy 3; Cy 5; Cy 5.5; Cy 7; IRD 700; IRD 800; La Jolla Blue; phthalo cyanine; and naphthalo cyanine.

101. A method for detecting multiple reiterated oligonucleotides from a target DNA or RNA polynucleotide, said method comprising:

(a) incubating a single-stranded target polynucleotide in a mixture comprising an initiator, and an RNA-polymerase;

(b) synthesizing multiple oligonucleotide transcripts from said target polynucleotide, wherein said initiator is extended until terminated due to nucleotide deprivation, thereby synthesizing multiple abortive reiterative oligonucleotide transcripts; and

(c) detecting or quantifying said reiteratively synthesized oligonucleotides

102. A method of detecting multiple reiterated oligonucleotides from a target DNA or RNA polynucleotide, said method comprising:

(a) incubating a single-stranded target polynucleotide in a mixture comprising an initiator, an RNA-polymerase, and a target site probe, wherein said target site probe and said target polynucleotide hybridize to form a bubble complex comprising a first double-stranded region upstream of a target site, a single-stranded region comprising said target site, and a second double-stranded region downstream of said target site;

(b) synthesizing multiple oligonucleotide transcripts from said target polynucleotide, wherein said initiator is extended until terminated due to nucleotide deprivation, thereby synthesizing multiple abortive reiterative oligonucleotides; and

(c) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts.

103. A method for detecting methylated cytosine residues at a CG site near a target gene, the method comprising:

(a) deaminating a single-stranded target DNA sequence under conditions which convert unmethylated cytosine residues to uracil residues while not converting methylated cytosine residues to uracil;

(b) incubating a single-stranded target polynucleotide in a mixture comprising an initiator, a terminator, an RNA-polymerase, and a target site probe;

(c) synthesizing multiple oligonucleotide transcripts from said target polynucleotide, wherein said initiator is extended until terminated due to nucleotide deprivation, thereby synthesizing multiple abortive reiterative oligonucleotide transcripts; and

(d) detecting or quantifying said reiteratively synthesized oligonucleotides

104. The method of claim 26 or 27, further comprising:

(a) immobilizing an oligonucleotide capture probe which is specific for a sequence near a CpG island related to a target gene; and

(b) hybridizing said oligonucleotide capture probe with a denatured DNA sample which potentially contains said target DNA sequence.

105. The method of claim 27, wherein said target site probe is gene specific cancer specific.

106. A method for detecting a target protein in a test sample, the method comprising:

(a) covalently attaching the target protein to an abortive promoter cassette (APC) by a reactive APC linker, wherein said APC comprises a region that can be detected by transcription by a polymerase;

(b) incubating said target protein with an RNA-polymerase, an initiator, and a terminator;

(c) synthesizing an oligonucleotide transcript that is complementary to transcription initiation start site of APC, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript, thereby synthesizing multiple reiterative oligonucleotide transcripts; and

(d) determining the presence or absence of the target protein by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts synthesized from said test sample.

107. The method of claim 106 further comprising immobilizing target protein by a target specific probe.

108. The method of claim 107, wherein said target specific probe is an antibody.

109. The method of claim 106, wherein said APC linker will be covalently attached to the target protein by modification of thiol-reactive or amine-reactive protein crosslinking agents.

110. The method of claim 109 wherein said protein crosslinking agents are selected from the group consisting of: maleamides, iodoacetamides, and disulfides.

111. The method of claim 106, wherein said target protein is purified or in a cell lysate.

112. A method for detecting cancer, comprising:

(a) obtaining a sample from a patient in need of detection of a cancer;

(b) deaminating the DNA under conditions which convert unmethylated cytosine residues to uracil residues while leaving the methylated cytosine residues unaltered;

(c) hybridizing an initiator to a target polynucleotide wherein said initiator is a mononucleoside, mononucleotide, binucleotide, oligonucleotide or an analog thereof;

(d) incubating said deaminated target polynucleotide and said initiator with a terminator, and an RNA-polymerase, wherein at least one of said initiator, terminator is modified to enable detection of the CG sites;

(e) synthesizing an oligonucleotide transcript that is complementary to said CG sites from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotide transcript thereby synthesizing multiple reiterative oligonucleotide transcripts;

(f) detecting or quantifying said reiteratively synthesized oligonucleotide transcripts; and

comparing the results with those obtained similarly from a control sample.

113. A method for detecting pathogens, said method comprising the steps of:

(a) obtaining a sample in need of detection of a pathogen

(b) hybridizing a single stranded target pathogen polynucleotide in said sample with an abortive promoter cassette comprising a nucleotide sequence that hybridizes to single stranded target pathogen polynucleotide, and a region that can be detected by transcription by a polymerase;

(c) incubating said target polynucleotide and initiator with an RNA-polymerase, and a terminator;

(d) synthesizing an oligonucleotide transcript that is complementary to initiation start site of the APC, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple abortive reiterative oligonucleotide transcripts; and

(e) determining the presence of a pathogen by detecting or quantifying said reiteratively synthesized oligonucleotide transcripts synthesized from said sample.

114. The method of claim 113, wherein said method further comprises:

(a) immobilizing an oligonucleotide capture probe which is specific for said target pathogen polynucleotide; and

(b) hybridizing said oligonucleotide capture probe with a denatured DNA sample which potentially contains said target pathogen polynucleotide.

115. A method for synthesizing multiple reiterated oligonucleotides from a target DNA or RNA polynucleotide, said method comprising:

(a) hybridizing an initiator with a single stranded target polynucleotide

(b) incubating said target polynucleotide and initiator with an RNA-polymerase, and a terminator;

(c) synthesizing multiple oligonucleotides from said target polynucleotide, wherein said initiator is extended until said terminator is incorporated into said oligonucleotides thereby synthesizing multiple reiterative oligonucleotides.

116. The method of claim 115, further comprising synthesizing oligonucleotides by modifying a nucleotide in at least one of the members selected from the group consisting of said terminator, and said initiator.

117. The method of claim 116, wherein said modifying comprises incorporating a label moiety.

118. The method of claim 117, wherein said label moiety comprises a fluorophore moiety.

119. The method of claim 118, wherein said fluorophore moiety comprises a fluorescent energy donor and a fluorescent energy acceptor .

120. The method of claim 115, wherein said polymerase is selected from the group consisting of: a DNA-dependent RNA polymerase, an RNA-dependent RNA polymerase and a modified RNA-polymerase, and a primase.

121. The method of claim 120, wherein said polymerase comprises an RNA polymerase derived from one of *E. coli, E. coli* bacteriophage T7, *E. coli* bacteriophage T3, and *S. typhimurium* bacteriophage SP6.

122. The method of claim 115, wherein said initiator comprises nucleotides selected from the group consisting of: 1-25 nucleotides, 26-50 nucleotides, 51-75 nucleotides, 76-100 nucleotides, 101-125 nucleotides, and 126-150 nucleotides, 151-175 nucleotides, 176-200 nucleotides, 201-225 nucleotides, 226-250 nucleotides, and greater than 250 nucleotides

123. The method of claim 115, wherein said abortive oligonucleotides being synthesized are one of the lengths selected from the group consisting of: about 2 to about 26 nucleotides, about 26 to about 50 nucleotides and about 50 nucleotides to about 100 nucleotides.

124. The method of claim 115, wherein said incubating further comprises a target site probe specific for a region on said single-stranded target polynucleotide.

125. The method of claim 115, wherein said chain terminator comprises a nucleotide analog.

126. The method of any one of claims 1, 13, 26, 27, 41, 54, 55, 56, 71, 72, 101, 102, 103, 106, 112, 113, or 115, wherein said incubating further comprises in the presence of ribonucleotides.

127. The method of claim 126, wherein said ribonucleotides are modified.

128. The method of claim 127, wherein said modifying further comprises incorporating an independently selected label moiety.

129. The method of claim 128, wherein said label moiety comprises a fluorophore moiety.

130. The method of claim 112 or 113, wherein said sample is obtained from the group consisting of: animal, plant or human tissue, blood, saliva, semen, urine, sera, cerebral or spinal fluid, pleural fluid, lymph, sputum, fluid from breast lavage, mucusoal secretions, animal solids, stool, cultures of microorganisms, liquid and solid food and feedproducts, waste, cosmetics, air and water.

131. The method of any one of claims 55, 56, 71, 72, 106, or 113, wherein said abortive promoter cassette comprises two partially complementary oligonucleotides that form a bubble region.

132. The method of any one of claims 55, 56, 71, 72, 106, or 113, wherein said abortive promoter cassette comprises two complementary oligonucleotides that form a bubble region in the presence of RNA polymerase.

133. The method of any one of claims 55, 56, 71, 72, 106, or 113, wherein said abortive promoter cassette comprises one contiguous oligonucleotide to which RNA polymerase can bind to form a transcription bubble.

134. The method of claim 59 wherein said fluorophore moiety is selected from the group consisting of: 4-acetamido-4'-isothiocyanatostilbene-2,2'disulfonic acid; acridine and derivatives: acridine, acridine isothiocyanate; 5-(2'-aminoethyl)amninonaphthalene-1-sulfonic acid (EDANS); 4-amino-N-[3-vinylsulfonyl)phenyl]naphthalimide-3,5 disulfonate; N-(4-amino-1-naphthyl)maleimide; anthranilamide; BODIPY; Brilliant Yellow; coumarin, and derivatives: coumarin, 7-amino-4-methylcoumarin (AMC, Coumarin 120), 7-amino-4-trifluoromethylcouluarin (Coumaran 151); cyanine dyes;

cyanosine; 4',6-diaminidino-2-phenylindole (DAPI); 5', 5"-dibromopyrogallol-sulfonaphthalein (Bromopyrogallol Red); 7-diethylamino-3-(4'-isothiocyanatophenyl)-4-methylcoumarin; diethylenetriamine pentaacetate; 4,4'-diisothiocyanatodihydro-stilbene-2,2'-disulfonic acid; 4,4'-diisothiocyanatostilbene-2,2'-disulfonic acid; 5-[dimethylamino]naphthalene-1-sulfonyl chloride (DNS, dansylchloride); 4-dimethylaminophenylazophenyl-4'-isothiocyanate (DABITC); eosin and derivatives: eosin, eosin isothiocyanate; erythrosin and derivatives: erythrosin B, erythrosin, isothiocyanate; ethidium; fluorescein and derivatives: 5-carboxyfluorescein (FAM),5-(4,6-dichlorotriazin-2-yl)aminofluorescein (DTAF), 2',7'-dimethoxy-4'5'-dichloro-6-carboxyfluorescein (JOE), fluorescein, fluorescein isothiocyanate, QFITC, (XRITC); fluorescamine; IR144; IR1446; Malachite Green isothiocyanate; 4-methylumbelliferoneortho cresolphthalein; nitrotyrosine; pararosaniline; Phenol Red; B-phycoerythrin; o-phthaldialdehyde; pyrene and derivatives: pyrene, pyrene butyrate, succinimidyl 1pyrene; butyrate quantum dots; Reactive Red 4; rhodamine and derivatives: 6-carboxy-X-rhodamine (ROX), 6-carboxyrhodamine (R6G), lissamine rhodamine B, sulfonyl chloride rhodamine (Rhod), rhodamine B, rhodamine 123, rhodamine X isothiocyanate, sulforhodamine B, sulforhodamine 101, sulfonyl chloride derivative of sulforhodamine 101 (Texas Red); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); tetramethyl rhodamine; tetramethyl rhodamine isothiocyanate (TRITC); riboflavin; rosolic acid; terbiun chelate derivatives; Cy 3; Cy 5; Cy 5.5; Cy 7; IRD 700; IRD 800; La Jolla Blue; phthalo cyanine; and naphthalo cyanine.

135. The method of any one of claims 1, 13, 26, 27, 41, 54-56, 71, 72, 85, 101-103, 106, 112, 113, or 115, wherein said initiator is selected from the group consisting of: nucleosides, nucleoside analogs, nucleotides, an nucleotide analogs.